



Divergence analysis and association of economical traits in Mustard (*Brassica juncea* L)

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The experiment was carried out to examine the genetic variability and contribution of some morphological characters for grain yield and oil %age. Twelve accessions of *Brassica juncea* were evaluated for correlation, metro-glyph and divergence analysis for genetic evaluation of the characters studied. Highly significant differences with considerable range of variability were observed among these genotypes for all the traits. Eight clusters had been made with different index scores. Highest genetic dissimilarity between Pak-85671 and RL-18 and lowest among UCD-83 and UCD-675 was observed. 1000-seed weight had the highest contribution to genetic divergence followed by Number of seeds per pod and Number of pods per plant; it was due to genetic dissimilarity among the genotypes for these traits. Number of secondary branches had no contribution to the total genetic divergence; this was due to genetic similarity among the genotypes for these traits.

INTRODUCTION

Mustard (*Brassica juncea* L.) is an important oilseed crop and is cultivated in hot regions of Russia, China, Canada and India with somewhat unreliable rainfall. It is considered to be natural amphidiploid (AABB) with chromosome number 36 (Axelson et al. 2000). It is an important source of edible oil in Pakistan. Local production of edible oil met only 14% of the country's requirement and remaining 86% is imported. The local production of edible oil was 0.462 million tonnes in Pakistan during 2015-16 which is not sufficient to meet the consumption (3.726 million tonnes). Consequently a huge amount of hard earned foreign exchange was spent on its import to meet the domestic requirements. Pakistan's import bill of edible oil during 2015-16 was Rs.284.546 billion (US\$2.710 billion). (Pakistan Economic Survey 2016-17) The main reason of low production is little attention on oilseed development and genetic improvement work. At the same time the demand is increasing due to rapid growing population and increasing per capita consumption (18kg) of edible oil (Pakistan Economic Survey 2016-17). The gap between production and consumption of edible oil is increasing year by year. It is necessary to take important measures to improve the production potential of domestic source of their traditional oilseeds. In view of the magnitude of edible oil shortage, the research and development work needs serious attentiveness. The improvement through breeding can be made successful by knowing the exact contribution of yield components of *Brassica* seed.

Brassica juncea is important oilseed crop in Pakistan due to early maturity, non-shattering type, heat and pest resistance. In Pakistan *Brassica juncea* is mostly grown for the purpose of edible oil (Mustafa

et al., 2017). Seed yield is quantitatively inherited trait and depends upon many other traits. These seed yield contributing traits are also inherited quantitatively. The contribution of these traits in seed yield is also influenced by environment (Yadava et al., 2011).

To study the interaction between two characters simple correlation analysis is used. A plant breeder should know about the importance of correlation because correlation shows the relationship between the different variables which are helpful in making decision in selection for breeding program (Engqvist & Becker, 1993).

In the perspective of afore explained situation the present study was planned to evaluate the quantitative characters which influence the yield. The accessions were tested for correlation, regression and divergence analysis of quantitative characters *Brassica juncea* which may lead to the improvement of these oleiferous oilseeds.

The study of yield and yield components through genetic correlations provide the information that how strongly these plant traits are genetically associated with one another. It permits the examination of association of various characters with yield. Thus estimation of genotypic and phenotypic correlation determines the yield components and as a result it paved the basis for selection of superior genotypes from the diverse breeding populations.

Metroglyph analysis (Anderson's Metroglyph) is a simple technique and is used for preliminary grouping of genotypes. With the help of this technique, one can easily predict genotypes which have high index scores and genotypes from different clusters can be crossed to have maximum variability of good combinations of characters. This information can be helpful to improve the desirable trait and in identifying and engineering the crosses that could be performed to obtain desired results.

Divergence analysis is a powerful tool in quantifying the degree of divergence at genotypic level. It quantifies the degree of divergence based on phenotypic observations in different crops. Literature showed

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that accessions from the same geographical region may differ genetically, phenotypically and in adaptability.

Therefore, the present study was undertaken to find *Brassica juncea* genetic variability, character association and contribution of yield and

quality related characters towards yield and quality and thereby to establish appropriate plant attributes for selection to improve the yield and quality status of *Brassica juncea* varieties in Pakistan.

Table 1 Genotypic (r_g) and phenotypic (r_p) correlation coefficient among nine characters of *Brassica juncea*

Characters	2	3	4	5	6	7	8	9	
1	0.65412	0.168	0.76902	-0.589	-0.4316	0.04253	-0.3451	-0.4686	r _g
	0.50595*	0.11744	0.56213*	-0.4255*	-0.367*	0.03062	-0.2899*	-0.4063*	r _p
2		1 0.37105	0.28482	0.26779	0.20154	0.2336	0.07841	0.2577	r _g
		1 0.3451*	0.17378	0.09311	0.14535	0.10336	0.06181	0.13619	r _p
3			1 0.4983	-0.1045	-0.0505	0.08382	0.7326	0.81981	r _g
			1 0.43234*	-0.0747	0.05295	0.5787*	0.54336*	0.56877*	r _p
4				1 -0.855	-0.0692	0.34242	-0.4132	-0.3232	r _g
				1 -0.6084	-0.0579	0.25265	-0.2647	-0.1692	r _p
5					1 0.63487	-0.4728	0.62629	0.55741	r _g
					1 0.45758*	-0.2826	0.42584*	0.46815*	r _p
6						1 -0.6709	0.8659	0.18926	r _g
						1 -0.4738*	0.33595*	0.0863	r _p
7							1 0.06603	0.6234	r _g
							1 0.04079	0.43068*	r _p
8								1 0.91704*	r _g
								1 0.61675*	r _p

Table 2 Cluster Number, index scores and Brassica genotypes included in each cluster

Cluster No	Genotype	Cluster Index
I	1,2,12	49
II	7,9	30
III	5,10	26
IV	3,6	24
V	11	11
VI	4	10
VII	8	10

Table 3 D² values in matrix form

Parents	2	3	4	5	6	7	8	9	10	11	12
1	40.36	109.307	95.080	32.823	47.072	121.124	141.902	56.089	27.905	32.203	37.781
2		42.363	57.505	11.804	4.320	52.236	93.901	42.781	20.323	12.831	27.232
3			20.489	28.262	34.075	10.638	23.907	29.849	44.582	45.985	132.340
4				22.952	42.052	39.734	9.857	47.819	52.853	48.838	145.781
5					7.611	44.108	50.904	29.770	14.879	11.891	57.343
6						49.268	73.735	48.387	19.283	9.988	44.984
7							42.882	30.027	57.471	62.638	141.089
8								61.167	89.332	87.905	207.907
9									24.152	36.682	95.926
10										7.385	50.850
11											43.383

Table 4 Contribution of each character to genetic divergence

Character	1	2	3	4	5	6	7	8	9	Total
First ranking	4	1	0	6	4	16	29	4	2	66
% contribution	6.06	1.52	0.00	9.09	6.06	24.24	43.94	6.06	3.03	100.0

RESULTS AND DISCUSSION

The results pertaining to analysis of variance elucidated significant differences among the accessions for all the traits and considerable range of variability. Association of plant height was negative and significant at genotypic as well as phenotypic level with seed yield per plant and seed yield per plot. Plant height was positively and significantly correlated with primary branches and number of pods per plant at both genotypic and phenotypic levels. Association of plant height with pod length, and number of seeds per pod was negative and significant at genotypic level but positive and non-significant with 1000-seed weight, negatively and significantly correlated at genotypic and phenotypic levels with seed yield per plant.

Primary branches positive and non-significant at both genotypic and phenotypic levels with seed yield per plant, number of pods per plant, 1000-seed weight, number of seeds per pod and pod length. Primary branches exhibit positive and significant correlation at genotypic and phenotypic levels with number of secondary branches per plant.

Association of secondary branches per plant with seed yield per plant was positive and significant and positive and high significance with 1000-seed weight and seed yield per plant. Negative and non-significant correlation with pod length and number of seeds per pod was examined.

Correlation between pods per plant and seed yield per plot was negative and significant at genotypic and non-significant at phenotypic

levels. Pods per plant were negative and non-significantly correlated with seeds per pod, seed yield per plant was negative and significant at genotypic and non-significant at phenotypic level. There is positive significant at genotypic and positive and non-significant at phenotypic level with 1000-seed weight.

Pod length has positive and highly significant correlation with yield per plot, number of seeds per pod and seed yield per plant at both genotypic and phenotypic levels. 1000-seed weight was negatively and significantly at genotypic and negatively and non-significantly at phenotypic level with pod length.

Positive and non-significant correlation between number of seeds per pod and seed yield per plot whereas negative and highly significant correlation with 1000-seed weight at both levels was observed. Positive and significant association with seed yield per plant was found.

1000-seed weight was positively and non-significantly correlated with seed yield per plant and exhibited positive and highly significant correlation at both genotypic and phenotypic levels with seed yield per plot.

Study manifested positive and highly significant correlation between seed yield per plant and seed yield per plot at both genotypic and phenotypic levels.

Labana *et al.* (1980) reported that plant height was negatively correlated with seed yield in *B. Juncea*. Chowdhury and Chowdhury (1970) showed that number of seeds per pod, number of pods per plant, 1000-seed weight and pod length had a non-significant and positive association with number of primary branches per plant. Khulbe and Pant (1999) reported positive and significant association between pod length and seed yield per plant in *B. Juncea*. Ikram-ul -Haq *et al.* (1998) and Masood *et al.* (1999) reported positive and significant correlation between seed yield per plant and seed yield per plot.

Seven clusters were obtained by Anderson's Metroglyph analysis (Table-2). Cluster I had genotypes UCD-8/4, UCD-83 and RL-18 with maximum index score 49. Cluster number II had genotypes UCD-7/8 and Pak-85642 with index score 30. Cluster III had genotype UCD-11/1 AND PLM-514 with index score 26. Cluster IV had two genotypes UCD-627 and UCD-675 with index score 24. Cluster V, VI and VII had single genotype each i.e. PAK-85648, UCD-323/2 and PAK-85671 with index score 11, 10 and 10 respectively.

Genetic divergence among the studied genotypes based on statistical differences was estimated by Mahalanobis's D^2 analysis (Table-3). In total 66 values of D^2 were calculated to know the genetic distance between twelve genotypes. The genetic dissimilarity was highest between PAK-85671 and RL-18 and was lowest among UCD-83 and UCD-675. It might be concluded that high D^2 value was due to genetic dissimilarity among genotypes and low D^2 value was due to genetic similarity among genotypes. UCD-83 was genetically similar to UCD-675 and PLM-514 was also genetically similar to Pak-85648.

Results in table-4 showed that the contribution of each character to the genetic divergence showed that 1000-seed weight had the highest contribution to genetic divergence (43.94%) followed by number of seeds per pod (24.24%), it was due to genetic dissimilarity among the genotypes for these traits. Number of secondary branches had no contribution (0.00%) to the total genetic divergence; this might be due to genetic similarity among the genotypes for these traits. Sandhu and Gupta (1996) investigated the genetic divergence for morphological quality attributes of three Brassica species, *B. juncea*, *B. napus* and *B. carinata*. The range of variation is highest in *B. juncea*. Gupta and Singh (1998) reported that genetic advance was greatest for yield per plant followed by plant height and number of branches. Mitra and Saini

(1998) evaluated forty three genotypes of toria and found no evidence for any correlation between genetic divergence and geographical diversity. The genotypes were grouped into seven clusters and also reported that genetic divergence was mainly contributed by number of secondary branches per plant, siliquae on the main shoot, seeds per siliquae and harvest index. Katiyar *et al.* (2000) concluded that there is adequate genetic divergence among Indian mustard lines to support a successful hybrid programme.

CONCLUSION

All the investigation in the present study proved quite successful because a handful increase in seed yield per plot is possible as they provide information regarding a suitable combination of characters with their maximum influence on the enhancement of seed yield per plot. The genotype will be selected with such combinations of characters which to give maximum improvement in their seed yield. 1000-seed weight, Number of seeds per pod and Number of pods per plant are major seed yield contributing traits in *Brassica juncea*. These traits must be focused during variety development program of Mustard.

MATERIALS AND METHODS

The present study was conducted in the experimental area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during 2014-15. Twelve accessions of *Brassica juncea* viz. UCD-8/4, UCD-83, UCD-627, UCD-323/2, UCD-11/1, UCD-675, UCD-7/8, Pak-85671, Pak-85642, PLM-514, Pak-85648 and RL-18 as standard. The accessions were laid out randomized complete block design with four replications. Plant to plant and row to row distances were 22 cm and 45 cm respectively. All the recommended agronomic practices were carried out in the field. At maturity, ten guarded plants were selected at random to record data. The data were recorded for plant height, number of primary branches, number of secondary branches, number of pods per plant, pod length, number of seeds per pod, 1000-seed weight, seed yield per plant and seed yield per plot.

At maturity, Plant height in cm was measured from ground level to tip of the plant including inflorescence by using meter rod. Number of primary and secondary branches of selected plants was counted. The total number of pods was counted in all the selected plants in each replication except seedless pods. The pod length was determined by measuring average length of ten randomly selected pods from each selected plant in each replication excluding the stalk of the pod and then average was calculated. A sample of ten pods of each selected plant was taken and average seeds per pod were collected and average of each sample of ten pods was taken for each selected plant from each plot in each replication. 1000-seed weight was determined in grams by counting 1000 seeds from selected plants from each accession and standard of each replication by using electronic balance. For seed yield per plant, pods were harvested and manually threshed separately and weighed in grams on digital electronic balance. Five middle rows of seven rowed plots of each accession were harvested and threshed separately, and the seed obtained from each plot was dried at room temperature and then weighed to obtain seed yield per plot under each replication.

Statistical Analysis

Genotypic and phenotypic correlation coefficients among the characters under study were estimated according to the statistical techniques outlined by Kown and Torrie (1964). Significance level was computed by using t-test as described by Steel *et al.* 1997. Divergence analysis was

determined according to Wilk's criterion (Singh & Chaudhary, 1985). Metroglyph analysis was performed as by Anderson's Metroglyph (1957). Clusters will be made by using Toucher's method (Rao, 1952).

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